CRF errors Corrected by the STIC Systems Branch   **ENTERED**

Serial Number: 09/756,983

CRF Processing Date: 2/13/2001
Edited by: _____
Verified by: _____ (STIC staff

S-140 OIPE

0400   02-8-1

- [ ] Changed a file from non-ASCII to ASCII
- [ ] Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- [ ] Edited a format error in the Current Application Data section, specifically: _____
- [x] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was [ ] the prior application data; or [ ] other _____   #2
- [ ] Added the mandatory heading and subheadings for "Current Application Data".
- [ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- [ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- [ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- [ ] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- [ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- [ ] Inserted colons after headings/subheadings. Headings edited included: _____
- [ ] Deleted extra, invalid, headings used by an applicant, specifically: _____
- [x] Deleted: [x] non-ASCII "garbage" at the beginning/end of files; [ ] secretary initials/filename at end of file; [ ] page numbers throughout text; [ ] other invalid text, such as _____
- [ ] Inserted mandatory headings, specifically: _____
- [ ] Corrected an obvious error in the response, specifically: _____
- [ ] Edited identifiers where upper case is used but lower case is required, or vice versa.
- [ ] Corrected an error in the Number of Sequences field, specifically: _____
- [ ] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- [ ] Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- [x] Other: *Seq. 1 - corrected amino acid numbering*
_____

EXaminer: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

#2

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/756,983

DATE: 02/13/2001
TIME: 08:41:47

Input Set : N:\Crf3\02052001\I756983.raw
Output Set: N:\CRF3\02132001\I756983.raw

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 1 <110> APPLICANT: Albani, Salvatore
 2 <120> TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
 3       CHARACTERIZATION AND MODULATION OF
 4       ANTIGEN-SPECIFIC T CELLS
 5 <130> FILE REFERENCE: 246/285-CIP
 6 <140> CURRENT APPLICATION NUMBER: US/09/756,983
 7 <141> CURRENT FILING DATE: 2001-01-09
 8 <150> PRIOR APPLICATION NUMBER: 60/105,018
 9 <151> PRIOR FILING DATE: 1998-10-20
10 <150> PRIOR APPLICATION NUMBER: 09/421,506
11 <151> PRIOR FILING DATE: 1999-10-19
12 <150> PRIOR APPLICATION NUMBER: PCT/US99/2466
13 <151> PRIOR FILING DATE: 1999-10-19
14 <160> NUMBER OF SEQ ID NOS: 24
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 17
19 <212> TYPE: PRT
20 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Synthesized peptide derived from third hyper V
23       region of IE molecule Mus musculus
24 <400> SEQUENCE: 1
25       Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys
26       1               5                   10                  15
27       Ala
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 15
31 <212> TYPE: PRT
32 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Synthesized peptide derived from bole I protein
35       of Epstein Barr virus
36 <400> SEQUENCE: 2
37       Thr Arg Asp Asp Ala Glu Tyr Leu Leu Gly Arg Glu Ser Val Leu
38       1               5                   10                  15
40 <210> SEQ ID NO: 3
41 <211> LENGTH: 16
42 <212> TYPE: PRT
43 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
45 <223> OTHER INFORMATION: Synthesized peptide derived from the hemophilus
46       influenza virus
47 <400> SEQUENCE: 3
48       Thr Ser Phe Pro Met Arg Gly Asp Leu Ala Lys Arg Glu Pro Asp Lys
49       1               5                   10                  15
51 <210> SEQ ID NO: 4
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RAW SEQUENCE LISTING   DATE: 02/13/2001
PATENT APPLICATION: US/09/756,983   TIME: 08:41:47

Input Set : N:\Crf3\02052001\I756983.raw
Output Set: N:\CRF3\02132001\I756983.raw

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52 <211> LENGTH: 36
53 <212> TYPE: PRT
54 <213> ORGANISM: Artificial Sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: Synthesized peptide derived from the TCR receptor
57       gene of Mus musculus
58 <400> SEQUENCE: 4
59       Leu His Ile Ser Ala Val Asp Pro Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser
60        1               5                  10                  15
61       Ser Gln Glu Phe Phe Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr
62           20              25                  30
63       Arg Leu
64        35
66 <210> SEQ ID NO: 5
67 <211> LENGTH: 9
68 <212> TYPE: PRT
69 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <223> OTHER INFORMATION: Synthesized peptide derived from the influenza virus
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74        1               5
76 <210> SEQ ID NO: 6
77 <211> LENGTH: 9
78 <212> TYPE: PRT
79 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Synthesized peptide derived from the influenza virus
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83       Val Lys Leu Gly Glu Phe Tyr Asn Gln
84        1               5
86 <210> SEQ ID NO: 7
87 <211> LENGTH: 11
88 <212> TYPE: PRT
89 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Synthesized peptide totally artificial
92 <223> OTHER INFORMATION: Xaa in position 2 stands for cyclohexylalanine
93 <400> SEQUENCE: 7
94       Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala
95        1               5                  10
97 <210> SEQ ID NO: 8
98 <211> LENGTH: 13
99 <212> TYPE: PRT
100 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Synthesized peptide derived from the influenza virus
103 <400> SEQUENCE: 8
104       Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/756,983

DATE: 02/13/2001
TIME: 08:41:47

Input Set : N:\Crf3\02052001\I756983.raw
Output Set: N:\CRF3\02132001\I756983.raw

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109 <212> TYPE: PRT
110 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Synthesized peptide derived from the ovalbumin
113      of Mus musculus
114 <400> SEQUENCE: 9
115      Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly
116       1             5                  10                 15
117      Arg
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120 <211> LENGTH: 15
121 <212> TYPE: PRT
122 <213> ORGANISM: E. coli
123 <220> FEATURE:
124 <223> OTHER INFORMATION: dnaJpl heat shock protein
125 <400> SEQUENCE: 10
126      Gln Lys Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu
127       1             5                  10                 15
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130 <211> LENGTH: 15
131 <212> TYPE: PRT
132 <213> ORGANISM: Homo sapiens
133 <400> SEQUENCE: 11
134      Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly
135       1             5                  10                 15
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138 <211> LENGTH: 9
139 <212> TYPE: PRT
140 <213> ORGANISM: Homo sapiens
141 <400> SEQUENCE: 12
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143       1             5
145 <210> SEQ ID NO: 13
146 <211> LENGTH: 9
147 <212> TYPE: PRT
148 <213> ORGANISM: Homo sapiens
149 <400> SEQUENCE: 13
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151       1             5
153 <210> SEQ ID NO: 14
154 <211> LENGTH: 13
155 <212> TYPE: PRT
156 <213> ORGANISM: Homo sapiens
157 <400> SEQUENCE: 14
158      Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
159       1             5                  10
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/756,983

DATE: 02/13/2001
TIME: 08:41:47

Input Set : N:\Crf3\02052001\I756983.raw
Output Set: N:\CRF3\02132001\I756983.raw

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162 <211> LENGTH: 313
163 <212> TYPE: PRT
164 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Fusion constructs with human and bacterial sequences
167 <400> SEQUENCE: 15
168     Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
169      1               5                  10                  15
170     Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
171                     20                  25                  30
172     Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
173                     35                  40                  45
174     Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
175             50                  55                  60
176     Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
177     65                  70                  75                  80
178     Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
179                     85                  90                  95
180     Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
181                     100                 105                 110
182     Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
183             115                 120                 125
184     Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
185             130                 135                 140
186     Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
187     145                 150                 155                 160
188     Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
189                     165                 170                 175
190     Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
191                     180                 185                 190
192     Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly
193             195                 200                 205
194     Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn
195             210                 215                 220
196     Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser
197     225                 230                 235                 240
198     Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala
199                     245                 250                 255
200     Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys
201                     260                 265                 270
202     Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr
203             275                 280                 285
204     Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His
205             290                 295                 300
206     Ala Ile Ala Ala Ile Ser Met Ala Asn
207     305                 310
209 <210> SEQ ID NO: 16
210 <211> LENGTH: 942
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212 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Fusion constructs with human and bacterial sequences
215 <400> SEQUENCE: 16
216        atgggccaca cacggaggca gggaacatca ccatccaagt gtccatacct caatttcttt 60
217        cagctcttgg tgctggctgg tctttctcac ttctgttcag gtgttatcca cgtgaccaag 120
218        gaagtgaaag aagtggcaac gctgtcctgt ggtcacaatg tttctgttga agagctggca 180
219        caaactcgca tctactggca aaaggagaag aaaatggtgc tgactatgat gtctggggac 240
220        atgaatatat ggcccgagta caagaaccgg accatctttg atatcactaa taacctctcc 300
221        attgtgatcc tggctctgcg cccatctgac gagggcacat acgagtgtgt tgttctgaag 360
222        tatgaaaaag acgctttcaa gcgggaacac ctggctgaag tgacgttatc agtcaaagct 420
223        gacttcccta cacctagtat atctyacttt gaaattccaa cttctaatat tagaaggata 480
224        atttgctcaa cctctggagg ttttccagag cctcacctct cctggttgga aaatggagaa 540
225        gaattaaatg ccatcaacac aacagtttcc caagatcctg aaactgagct ctatgctgtt 600
226        agcgaattcg gcggctccgg tggtagcgcc acacctcaaa atattactga tttgtgtgca 660
227        gaataccaca acacacaaat acatacgcta aatgataaga tattttcgta tacagaatct 720
228        ctagctggaa aaagagagat ggctatcatt acttttaaga atggtgcaac ttttcaagta 780
229        gaagtaccag gtagtcaaca tatagattca caaaaaaaag cgattgaaag gatgaaggat 840
230        accctgagga ttgcatatct tactgaagct aaagtcgaaa agttatgtgt atggaataat 900
231        aaaacgcctc atgcg:ttgc cgcaattagt atggcaaatt aa                      942
233 <210> SEQ ID NO: 17
234 <211> LENGTH: 1056
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Fusion constructs with human and bacterial sequences
239 <400> SEQUENCE: 17
240        atgggactga gtaacattct ctttgtgatg gccttcctgc tctctggtgc tgctcctctg 60
241        aagattcaag cttatttcaa tgagactgca gacctgccat gccaatttgc aaactctcaa 120
242        aaccaaagcc tgagtgagct agtagtattt tggcaggacc aggaaaactt ggttctgaat 180
243        gaggtatact taggcaaaga gaaatttgac agtgttcatt ccaagtatat gggccgcaca 240
244        agttttgatt cggacagttg gaccctgaga cttcacaatc ttcagatcaa ggacaagggc 300
245        ttgtatcaat gtatcatcca tcacaaaaag cccacaggaa tgattcgcat ccaccagatg 360
246        aattctgaac tgtcagtgct tgctaacttc agtcaacctg aaatagtacc aatttctaat 420
247        ataacagaaa atgtgtacat aaatttgacc tgctcatcta tacacggtta cccagaacct 480
248        aagaagatga gtgtttttgct aagaaccaag aattcaacta tcgagtatga tggtattatg 540
249        cagaaatctc aagataatgt cacagaactg tacqacgttt ccatcagctt gtctgtttca 600
250        ttccctgatg ttacgagcaa tatgaccatc ttctgtattc tggaaactga caagacgcgg 660
251        ctttttatctt caccttctc tatagagctt gaggaccctc agcctccccc agaccacgaa 720
252        ttcggcggct ccggtggtag cgccacacct caaatatta ctgatttgtg tgcagaatac 780
253        cacaacacac aaatacatac gctaaatgat aagatatttt cgtatacaga atctctagct 840
254        ggaaaagag agatggctat cattactttt aagaatggtg caactttca agtagaagta 900
255        ccaggtagtc aacatataga ttcacaaaaa aaagcgattg aaaggatgaa ggataccctg 960
256        aggattgcat atcttactga agctaaagtc gaaaagttat gtgtatggaa taataaaacg 1020
257        cctcatgcga ttgccgcaat tagtatggca aattaa                           1056
259 <210> SEQ ID NO: 18
260 <211> LENGTH: 351
261 <212> TYPE: PRT
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VERIFICATION SUMMARY   DATE: 02/13/2001
PATENT APPLICATION: US/09/756,983   TIME: 08:41:48

Input Set : N:\Crf3\02052001\I756983.raw
Output Set: N:\CRF3\02132001\I756983.raw

L:94 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:94 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:94 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7

OIPE

RAW SEQUENCE LISTING   DATE: 02/13/2001
PATENT APPLICATION: US/09/756,983   TIME: 08:09:09

    Input Set : N:\Crf3\02052001\I756983.raw
    Output Set: N:\CRF3\02132001\I756983.raw

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 1 <110> APPLICANT: Albani, Salvatore
 2 <120> TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
 3       CHARACTERIZATION AND MODULATION OF
 4       ANTIGEN-SPECIFIC T CELLS
 5 <130> FILE REFERENCE: 246/285-CIP
 6 <140> CURRENT APPLICATION NUMBER: US/09/756,983
 7 <141> CURRENT FILING DATE: 2001-01-09
 8 <150> PRIOR APPLICATION NUMBER: 60/105,018
 9 <151> PRIOR FILING DATE: 1998-10-20
10 <150> PRIOR APPLICATION NUMBER: 09/421,506
11 <151> PRIOR FILING DATE: 1999-10-19
12 <150> PRIOR APPLICATION NUMBER: PCT/US99/2466
13 <151> PRIOR FILING DATE: 1999-10-19
14 <160> NUMBER OF SEQ ID NOS: 24
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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ERRORED SEQUENCES

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17 <210> SEQ ID NO: 1
18 <211> LENGTH: 17
19 <212> TYPE: PRT
20 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Synthesized peptide derived from third hyper V
23       region of IE molecule Mus musculus
24 <400> SEQUENCE: 1
25       Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys
E--> 26      1   5                  10                  15
27       Ala
439 <210> SEQ ID NO: 24
440 <211> LENGTH: 285
441 <212> TYPE: PRT
442 <213> ORGANISM: Artificial Sequence
443 <220> FEATURE:
444 <223> OTHER INFORMATION: Fusion constructs with human and bacterial sequences
445 <400> SEQUENCE: 24
446       Met Val Cys Leu Lys Phe Pro Gly Gly Ser Cys Met Ala Ala Leu Thr
447        1               5                  10                  15
448       Val Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr
449                       20                  25                  30
450       Arg Pro Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn
451                       35                  40                  45
452       Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu
453                   50                  55                  60
454       Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr
455       65                  70                  75                  80
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misaligned

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456        Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
457                        85              90              95
458        Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr
459                        100             105             110
460        Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val
461                115             120             125
462        Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
463                130             135             140
464        Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
465        145             150             155             160
466        Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser Thr Gly Leu
467                165             170             175
468        Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr
469                180             185             190
470        Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
471                195             200             205
472        Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
473                210             215             220
474        Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu
475        225             230             235             240
476        Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala
477                245             250             255
478        Leu Lys Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly
479                260             265             270
480        Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
481                275             280             285
E--> 482  1
E--> 483  2
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VERIFICATION SUMMARY   DATE: 02/13/2001
PATENT APPLICATION: US/09/756,983   TIME: 08:09:10

Input Set : N:\Crf3\02052001\I756983.raw
Output Set: N:\CRF3\02132001\I756983.raw

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L:26  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:94  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:94  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:94  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:482 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24
M:332 Repeated in SeqNo=24
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